

Sequence alignment for 10/527,469

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US-08-813-150-4
; Sequence 4, Application US/08813150
; Patent No. 6069229
; GENERAL INFORMATION:
; APPLICANT: Mueller, Christopher
; APPLICANT: Lebecque, Serge J.E.
; APPLICANT: Liu, Yong-Jun
; APPLICANT: Dowling, Lynette M.
; APPLICANT: Huffine, Constance M.
; APPLICANT: Gorman, Daniel M.
; TITLE OF INVENTION: MAMMALIAN PROTEINASES; OXIDOREDUCTASES;
; TITLE OF INVENTION: RELATED REAGENTS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/813,150
; FILING DATE: 07-MAR-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: SF0693
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-852-9196
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; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 567 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-813-150-4

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Query Match 100.0%; Score 567; DB 2; Length 567;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 567; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MAPLALHLLVLPILLSLVSQDWKAERSQDPFEKCMQDPDYEQLLKVVVTWGLNRTLKPQ	60
Db	1	MAPLALHLLVLPILLSLVSQDWKAERSQDPFEKCMQDPDYEQLLKVVVTWGLNRTLKPQ	60
Qy	61	RVIVVGAGVAGLVAAKVLSDAGHKVTILEADNRIGGRIFTYRDQNTGWIGELGAMRMPSS	120
Db	61	RVIVVGAGVAGLVAAKVLSDAGHKVTILEADNRIGGRIFTYRDQNTGWIGELGAMRMPSS	120
Qy	121	HRILHKLCQGLGLNLTKFTQYDKNTWTEVHEVKLRNYVVEKVPEKLGALRPOEKGHSPE	180
Db	121	HRILHKLCQGLGLNLTKFTQYDKNTWTEVHEVKLRNYVVEKVPEKLGALRPOEKGHSPE	180

Qy	181	DIYQMALNQALKDLKALGCRKAMKKFERHTLLEYLLGEGNLSRPAVQLLDGDMSEDGFFY	240
Db	181	DIYQMALNQALKDLKALGCRKAMKKFERHTLLEYLLGEGNLSRPAVQLLDGDMSEDGFFY	240
Qy	241	LSFAEALRAHSCLSDRLQYSRIVGGWDLPRALLSSLSGLVLLNAPVVAMTQGPHDVHVQ	300
Db	241	LSFAEALRAHSCLSDRLQYSRIVGGWDLPRALLSSLSGLVLLNAPVVAMTQGPHDVHVQ	300
Qy	301	IETSPPARNLKVLKADVLLTASGPAVKRITFSPPLPRHMQEALRRLHYVPATKVFLSFR	360
Db	301	IETSPPARNLKVLKADVLLTASGPAVKRITFSPPLPRHMQEALRRLHYVPATKVFLSFR	360
Qy	361	RPFWREEHIEGGHSNTDRPSRMIFYPPPREGALLASYTWSDAAAFAGLSREEALRLAL	420
Db	361	RPFWREEHIEGGHSNTDRPSRMIFYPPPREGALLASYTWSDAAAFAGLSREEALRLAL	420
Qy	421	DDVAALHGPVVRQLWDGTGVVKRWAEDQHSQGGFVVQPPALWQTEKDDWTVPYGRIYFAG	480
Db	421	DDVAALHGPVVRQLWDGTGVVKRWAEDQHSQGGFVVQPPALWQTEKDDWTVPYGRIYFAG	480
Qy	481	EHTAYPHGWVETAVKSALRAAIKINSRKGPASDTASPEGHASDMEGQGHVHGVASSPSHD	540
Db	481	EHTAYPHGWVETAVKSALRAAIKINSRKGPASDTASPEGHASDMEGQGHVHGVASSPSHD	540
Qy	541	LAKEEGSHPPVQGQLSLQNTTHTRTSH	567
Db	541	LAKEEGSHPPVQGQLSLQNTTHTRTSH	567